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**AMENDMENT**

Please amend the application without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, as follows.

**In the Claims**

1. (Previously presented) The isolated and purified retrotransposon according to claim 12 comprising the gag and pol ORF in the same phase and found as an extrachromosomal DNA molecule having a copy number of 40-150 free DNA copies per cell in *Candida albicans*.
2. (Previously presented) The retrotransposon according to claim 12 which is linear.
3. (Previously presented) The retrotransposon according to claim 2 which is double stranded.
4. (Previously presented) The retrotransposon according to claim 12 which is isolated from fungi or yeast.
5. (Currently amended) ~~The~~ An isolated retrotransposon ~~according to any one of claims 12, 1 or 4~~ consisting of SEQ ID NO:3.
- 6-9. (Cancelled)
10. (Currently amended) The DNA transfer construct according to claim 17 ~~or claim~~ 51 comprising:
  - a) a transposable element for introducing a desired DNA sequence into the genome of a cell, having the sequence identified in SEQ ID NO:3 comprising an internal domain for receiving a nucleotide sequence encoding a desired protein, said internal domain comprising the gag and pol ORF in the same phase and flanked by two terminal repeat regions, said transposable element being capable of integrating into the genome of a cell in the presence of an integration factor; and
  - b) a nucleotide sequence encoding an integration factor.
11. (Previously presented) The DNA transfer construct according to claim 10, wherein the integration factor is an integrase protein encoded by a nucleotide sequence within the pol ORF of the DNA transfer construct.
12. (Currently amended) An isolated and purified retrotransposon comprising a nucleotide sequence which has at least 95% sequence similarity with a nucleotide sequence selected from the group consisting of:

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- (a) SEQ ID NO:3; ~~and~~
  - (b) the LTR and POL region of SEQ ID NO:3; ~~and~~
  - (c) ~~a nucleotide sequence that hybridizes under stringent conditions to SEQ ID NO:3.~~
13. (Currently amended) ~~The retrotransposon claimed in claim 12, consisting of A~~  
cell transformed with TCa2, wherein TCa2 the isolated and purified retrotransposon is integrated  
into the genome of [[a]] the cell.
14. (Currently amended) An expression vector comprising the retrotransposon of  
claim ~~1, 4, 5 or 12.~~
15. (Cancelled)
16. (Cancelled)
17. (Currently amended) A DNA transfer construct comprising the retrotransposon of  
claim ~~1, 4, 5, or 12.~~
18. (Cancelled)
19. (Currently amended) An isolated nucleic acid fragment selected from the group  
consisting of:
- (a) a nucleic acid sequence positioned between comprising two terminal repeats of  
the sequence of pCal, as described in GenBank accession number AF007776, and a nucleic acid  
molecule of interest, wherein the nucleic acid molecule of interest is positioned between the two  
terminal repeats; and
  - (b) a nucleic acid sequence consisting of the LTR and POL region of SEQ ID NO:3;  
and
  - (c) ~~a nucleic acid sequence that hybridizes under stringent conditions to the~~  
~~nucleotide sequence of (a).~~
20. (Previously presented) The nucleic acid fragment according to claim 19 in which  
the nucleic acid sequence comprises a functional POL gene.
21. (Previously presented) The nucleic acid fragment according to claim 19 in which  
the nucleic acid sequence comprises a series of genes in the order gag (group antigen), pol  
(polyprotein) where the pol sequence comprises an aspartic protease, an integrase and a reverse  
transcriptase/RNaseII.
- 22-34. (Cancelled)

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35. (Currently amended) The retrotransposon of ~~claims 1, 4, 5 or~~ claim 12, wherein the retrotransposon comprises a nucleotide sequence having four tandem repeats of the sequence GAAAAA.

36. (Previously presented) The DNA transfer vector of claim 17, wherein the transposable element comprises a nucleotide sequence having four tandem repeats of the sequence GAAAAA.

37. (Previously presented) The retrotransposon of claim 12, wherein the nucleotide sequence of (b) has at least 70% similarity with the LTR and POL region of SEQ ID NO:3.

38. (Previously presented) The retrotransposon of claim 12, wherein the nucleotide sequence of (b) has at least 75% similarity with the LTR and POL region of SEQ ID NO:3.

39. (Previously presented) The retrotransposon of claim 12, wherein the nucleotide sequence of (b) has at least 80% similarity with the LTR and POL region of SEQ ID NO:3.

40. (Previously presented) The retrotransposon of claim 12, wherein the nucleotide sequence of (b) has at least 85% similarity with the LTR and POL region of SEQ ID NO:3.

41. (Previously presented) The retrotransposon of claim 12, wherein the nucleotide sequence of (b) has at least 90% similarity with the LTR and POL region of SEQ ID NO:3.

42. (Previously presented) The retrotransposon of claim 12, wherein the nucleotide sequence of (b) has at least 95% similarity with the LTR and POL region of SEQ ID NO:3.

43. (Previously presented) The retrotransposon of claim 12, wherein the nucleotide sequence of (b) has at least 97% similarity with the LTR and POL region of SEQ ID NO:3.

44. (Previously presented) The nucleic acid fragment of claim 19, wherein the nucleic acid sequence of (b) has at least 70% similarity with the LTR and POL region of the sequence of (a).

45. (Previously presented) The nucleic acid fragment of claim 19, wherein the nucleic acid sequence of (b) has at least 75% similarity with the LTR and POL region of the sequence of (a).

46. (Previously presented) The nucleic acid fragment of claim 19, wherein the nucleic acid sequence of (b) has at least 80% similarity with the LTR and POL region of the sequence of (a).

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47. (Previously presented) The nucleic acid fragment of claim 19, wherein the nucleic acid sequence of (b) has at least 85% similarity with the LTR and POL region of the sequence of (a).

48. (Previously presented) The nucleic acid fragment of claim 19, wherein the nucleic acid sequence of (b) has at least 90% similarity with the LTR and POL region of the sequence of (a).

49. (Previously presented) The nucleic acid fragment of claim 19, wherein the nucleic acid sequence of (b) has at least 95% similarity with the LTR and POL region of the sequence of (a).

50. (Previously presented) The nucleic acid fragment of claim 19, wherein the nucleic acid sequence of (b) has at least 97% similarity with the LTR and POL region of the sequence of (a).

51. (Previously presented) The DNA transfer construct of claim 17, further comprising a dominant selectable marker.